


# Appendix I

## Alignment of instant SEQ ID NO: 1 and BAA23691.2 (KIAA0395)


 BAA23691.2 KIAA0395 [Homo sapiens]  
 Length=879

Score = 1829 bits (4738), Expect = 0.0, Method: Compositional matrix adjust.  
 Identities = 878/879 (99%), Positives = 878/879 (99%), Gaps = 0/879 (0%)

Query	78	SCKYCDFRSHDMTQFVGHMNSHHTDFNKKDPTTFCGCGSLAKTPEGLSLHNATCHSGEAS	137
Shjet	1	SCKYCDFRSHDMTQFVGHMNSHHTDFNKKDPTTFCGCGSLAKTPEGLSLHNATCHSGEAS	60
Query	138	FVWVNAKPDNHVVVEQSIPSTSTPDLAGEPSARGADGQAEIIITKTPIMKIMKGKARAK	197
Shjet	61	FVWVNAKPDNHVVVEQSIPSTSTPDLAGEPSARGADGQAEIIITKTPIMKIMKGKARAK	120
Query	198	KIHTLKENVPSQFVGAEALFKLSTGEMEVREGDHSFINGAVFVSQASASSAKNPHAANGFL	257
Shjet	121	KIHTLKENVPSQFVGAEALFKLSTGEMEVREGDHSFINGAVFVSQASASSAKNPHAANGFL	180
Query	258	IGTVVLPAGIAQFLSLQQQPFVHAQHHVHQLPETAALPKVMIPLESSIPTTHAAMDSENS	317
Shjet	181	IGTVVLPAGIAQFLSLQQQPFVHAQHHVHQLPETAALPKVMIPLESSIPTTHAAMDSENS	240
Query	318	FLKNSFHKFPFPTKAECLYLTVVTKYPEQLKIMPTAQGLKQGISWSPEEIEHAPKMFN	377
Shjet	241	FLKNSFHKFPFPTKAECLYLTVVTKYPEQLKIMPTAQGLKQGISWSPEEIEHAPKMFN	300
Query	378	TVIQVPOPTITVLNTPFLVASAGNVQHLIQAAALPGHVVGQPEGTGGGLLVTOPLMANGLO	437
Shjet	301	TVIQVPOPTITVLNTPFLVASAGNVQHLIQAAALPGHVVGQPEGTGGGLLVTOPLMANGLO	360
Query	438	ATSSPFLPLTVTSVPKQGVAPINTVCSNITTSVAVKVVNAQSGLLTACPSITSQAFLDASIY	497
Shjet	361	ATSSPFLPLTVTSVPKQGVAPINTVCSNITTSVAVKVVNAQSGLLTACPSITSQAFLDASIY	420
Query	498	KNKSHHEQLSALKGSFCRNQFPQGSVEVHLTKVTLSTREVRNPSDRRIHCRNLKGSRA	557
Shjet	421	KNKSHHEQLSALKGSFCRNQFPQGSVEVHLTKVTLSTREVRNPSDRRIHCRNLKGSRA	480
Query	558	MIPGDHSSIIIDSVPVSVSPSSKVPVETCIPITATLATHPSAKRQSMWQTPFPFTTKYK	617
Shjet	481	MIPGDHSSIIIDSVPVSVSPSSKVPVETCIPITATLATHPSAKRQSMWQTPFPFTTKYK	540
Query	618	ERAPQLRALSSFAQNPLPLDELDRLRSETKMTREIDSWFSERPKVNAEETTKAEZ	677
Shjet	541	ERAPQLRALSSFAQNPLPLDELDRLRSETKMTREIDSWFSERPKVNAEETTKAEZ	600
Query	678	MAEQEEEAAREDEGGEEDLASELTVSGENGSLMPSSHILAEKRVSPIKIHLNKLNVTEA	737
Shjet	601	MAEQEEEAAREDEGGEEDLASELTVSGENGSLMPSSHILAEKRVSPIKIHLNKLNVTEA	660
Query	738	NGRNEIFGLGACDFEDDESCKLAELPGKVCCKTKAQRRHLRLQFVQGMPSNQYDSI	797
Shjet	661	NGRNEIFGLGACDFEDDESCKLAELPGKVCCKTKAQRRHLRLQFVQGMPSNQYDSI	720
Query	798	MACTGLERPEVVRWFQDSRYALKNSQLKMYEDYKRGNFPFGLLVIAPEGRELLQDYVYMT	857
Shjet	721	MACTGLERPEVVRWFQDSRYALKNSQLKMYEDYKRGNFPFGLLVIAPEGRELLQDYVYMT	780
Query	858	KMLYEELQNLCDKTQMSQQVQKQWFAEKMGEEETRAVADTGSDEQGPCTELTAVHKGMS	917
Shjet	781	KMLYEELQNLCDKTQMSQQVQKQWFAEKMGEEETRAVADTGSDEQGPCTELTAVHKGMS	840
Query	918	DTYSEVSENSESWEPVPEASSEFFDTSSPOAGRQLETD	956
Shjet	841	DTYSEVSENSESWEPVPEASSEFFDTSSPOAGRQLETD	879